

Rec'd PCT/PT

RAW SEQUENCE LISTING

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Application Serial Number: 10/518,884
Source: PT
Date Processed by STIC: 3/3/06

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Rec'd PCT/PTO 08 SEP 2005



PCT

RAW SEQUENCE LISTING

DATE: 03/03/2006

PATENT APPLICATION: US/10/518,884

TIME: 12:57:49

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Output Set: N:\CRF4\03032006\J518884.raw

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3 <110> APPLICANT: Martin, Catherine R
4     Michael, Anthony
5     Niggeweg, Ricarda
7 <120> TITLE OF INVENTION: Plant-Derived Transferase Genes
9 <130> FILE REFERENCE: 0380-P03542US0
11 <140> CURRENT APPLICATION NUMBER: US 10/518,884
12 <141> CURRENT FILING DATE: 2004-12-20
14 <150> PRIOR APPLICATION NUMBER: PCT/GB2003/002645
15 <151> PRIOR FILING DATE: 2003-06-17
17 <150> PRIOR APPLICATION NUMBER: GB 0214406.1
18 <151> PRIOR FILING DATE: 2002-06-21
20 <160> NUMBER OF SEQ ID NOS: 23
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 430
26 <212> TYPE: PRT
27 <213> ORGANISM: Lycopersicon esculentum
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35 Val Lys Pro Ser Lys Pro Thr Pro Thr Lys Arg Ile Trp Ser Ser Asn
36           20           25           30
39 Leu Asp Leu Ile Val Gly Arg Ile His Leu Leu Thr Val Tyr Phe Tyr
40           35           40           45
43 Lys Pro Asn Gly Ser Ser Asn Phe Phe Asp Asn Lys Val Ile Lys Glu
44           50           55           60
47 Ala Leu Ser Asn Val Leu Val Ser Phe Tyr Pro Met Ala Gly Arg Leu
48 65           70           75           80
51 Gly Arg Asp Glu Gln Gly Arg Ile Glu Val Asn Cys Asn Gly Glu Gly
52           85           90           95
55 Val Leu Phe Val Glu Ala Glu Ser Asp Ser Cys Val Asp Asp Phe Gly
56           100          105          110
59 Asp Phe Thr Pro Ser Leu Glu Leu Arg Lys Leu Ile Pro Ser Val Glu
60           115          120          125
63 Thr Ser Gly Asp Ile Ser Thr Phe Pro Leu Val Ile Phe Gln Ile Thr
64           130          135          140
67 Arg Phe Lys Cys Gly Gly Val Ala Leu Gly Gly Gly Val Phe His Thr
68 145          150          155          160
71 Leu Ser Asp Gly Leu Ser Ser Ile His Phe Ile Asn Thr Trp Ser Asp
72           165          170          175
75 Ile Ala Arg Gly Leu Ser Val Ala Val Pro Pro Phe Ile Asp Arg Thr
76           180          185          190
79 Leu Leu Arg Ala Arg Asp Pro Pro Thr Tyr Ser Phe Glu His Val Glu

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80          195          200          205
83 Tyr His Pro Pro Pro Thr Leu Asn Ser Ser Lys Asn Arg Glu Ser Ser
84          210          215          220
87 Thr Thr Thr Met Leu Lys Phe Ser Ser Glu Gln Leu Gly Leu Leu Lys
88 225          230          235          240
91 Ser Lys Ser Lys Asn Glu Gly Ser Thr Tyr Glu Ile Leu Ala Ala His
92          245          250          255
95 Ile Trp Arg Cys Thr Cys Lys Ala Arg Gly Leu Pro Glu Asp Gln Leu
96          260          265          270
99 Thr Lys Leu His Val Ala Thr Asp Gly Arg Ser Arg Leu Cys Pro Pro
100          275          280          285
103 Leu Pro Pro Gly Tyr Leu Gly Asn Val Val Phe Thr Ala Thr Pro Ile
104          290          295          300
107 Ala Lys Ser Cys Glu Leu Gln Ser Glu Pro Leu Thr Asn Ser Val Lys
108 305          310          315          320
111 Arg Ile His Asn Glu Leu Ile Lys Met Asp Asp Asn Tyr Leu Arg Ser
112          325          330          335
115 Ala Leu Asp Tyr Leu Glu Leu Gln Pro Asp Leu Ser Thr Leu Ile Arg
116          340          345          350
119 Gly Pro Ala Tyr Phe Ala Ser Pro Asn Leu Asn Ile Asn Ser Trp Thr
120          355          360          365
123 Arg Leu Pro Val His Glu Cys Asp Phe Gly Trp Gly Arg Pro Ile His
124          370          375          380
127 Met Gly Pro Ala Cys Ile Leu Tyr Glu Gly Thr Ile Tyr Ile Ile Pro
128 385          390          395          400
131 Ser Pro Asn Ser Lys Asp Arg Asn Leu Arg Leu Ala Val Cys Leu Asp
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141 <212> TYPE: PRT
142 <213> ORGANISM: Nicotiana tabacum
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151          20          25          30
154 Leu Asp Leu Ile Val Gly Arg Ile His Leu Leu Thr Val Tyr Phe Tyr
155          35          40          45
158 Lys Pro Asn Gly Ser Ser Asn Phe Phe Asp Ser Lys Ile Met Lys Glu
159          50          55          60
162 Ala Leu Ser Asn Val Leu Val Ser Phe Tyr Pro Met Ala Gly Arg Leu
163 65          70          75          80
166 Ala Arg Asp Glu Gln Gly Arg Ile Glu Ile Asn Cys Asn Gly Glu Gly
167          85          90          95
170 Val Leu Phe Val Glu Ala Glu Ser Asp Ala Phe Val Asp Asp Phe Gly
171          100          105          110
174 Asp Phe Thr Pro Ser Leu Glu Leu Arg Lys Leu Ile Pro Thr Val Asp

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175          115          120          125
178 Thr Ser Gly Asp Ile Ser Thr Phe Pro Leu Ile Ile Phe Gln Val Thr
179          130          135          140
182 Arg Phe Lys Cys Gly Gly Val Ser Leu Gly Gly Gly Val Phe His Thr
183 145          150          155          160
186 Leu Ser Asp Gly Leu Ser Ser Ile His Phe Ile Asn Thr Trp Ser Asp
187          165          170          175
190 Ile Ala Arg Gly Leu Ser Val Ala Ile Pro Pro Phe Ile Asp Arg Thr
191          180          185          190
194 Leu Leu Arg Ala Arg Asp Pro Pro Thr Ser Ser Phe Glu His Val Glu
195          195          200          205
198 Tyr His Pro Pro Pro Ser Leu Ile Ser Ser Ser Lys Ser Leu Glu Ser
199          210          215          220
202 Thr Ser Pro Lys Pro Ser Thr Thr Thr Met Leu Lys Phe Ser Ser Asp
203 225          230          235          240
206 Gln Leu Gly Leu Leu Lys Ser Lys Ser Lys His Asp Gly Ser Thr Tyr
207          245          250          255
210 Glu Ile Leu Ala Ala His Ile Trp Arg Cys Thr Cys Lys Ala Arg Ala
211          260          265          270
214 Leu Ser Asp Asp Gln Leu Thr Lys Leu His Val Ala Thr Asp Gly Arg
215          275          280          285
218 Ser Arg Leu Cys Pro Pro Leu Pro Pro Gly Tyr Leu Gly Asn Val Val
219          290          295          300
222 Phe Thr Gly Thr Pro Met Ala Lys Ser Ser Glu Leu Leu Gln Glu Pro
223 305          310          315          320
226 Leu Thr Asn Ser Ala Lys Arg Ile His Ser Ala Leu Ser Lys Met Asp
227          325          330          335
230 Asp Asn Tyr Leu Arg Ser Ala Leu Asp Tyr Leu Glu Leu Leu Pro Asp
231          340          345          350
234 Leu Ser Ala Leu Ile Arg Gly Pro Thr Tyr Phe Ala Ser Pro Asn Leu
235          355          360          365
238 Asn Ile Asn Ser Trp Thr Arg Leu Pro Val His Asp Ser Asp Phe Gly
239          370          375          380
242 Trp Gly Arg Pro Ile His Met Gly Pro Ala Cys Ile Leu Tyr Glu Gly
243 385          390          395          400
246 Thr Val Tyr Ile Leu Pro Ser Pro Asn Ser Lys Asp Arg Asn Leu Arg
247          405          410          415
250 Leu Ala Val Cys Leu Asp Ala Asp His Met Pro Leu Phe Glu Lys Tyr
251          420          425          430
254 Leu Tyr Glu Phe
255          435
258 <210> SEQ ID NO: 3
259 <211> LENGTH: 1456
260 <212> TYPE: DNA
261 <213> ORGANISM: Nicotiana tabacum
263 <400> SEQUENCE: 3
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266 aaaccaacac caacaaaaag actttggagt tctaacttag atttaatagt gggaagaatt 120
268 catcttttaa cagtatatatt ctataaacca aatggatctt caaatttctt tgattcaaaa 180

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270 ataatgaaag aagcattaag taatgttctt gtttcatttt acccaatggc tggagatta 240
272 gctagagatg aacaaggaag aattgagata aattgtaatg gagaaggagt tttatttggt 300
274 gaagctgaaa gtgatgcttt tgttgatgat tttggtgatt ttactccaag tttggaactt 360
276 aggaaactta ttctactgtg tgacacttct ggtgatattt ctactttccc cctcatcatc 420
278 tttcagggtta ctcgtttcaa atgtggtgga gtttcacttg gtggaggagt attccacact 480
280 ttatcagatg gtctctcatc aattcacttc atcaacacat ggtccgatat agcccagggc 540
282 ctctccgtcg ccatcccgcc gttcatcgac cggaccctcc tccgtgcacg ggaccacca 600
284 acatcgctct tgcagcacgt cgagtatcat cctcctccat ctctaatttc atcatcaaaa 660
286 agcttagaat ccactagccc aaagcctagt accacaacca tgttaaaatt ctctagtgcg 720
288 caacttgggc ttctaaagtc caagtccaaa catgatggtg gcacttacga aatcctcgcg 780
290 gcccatattt ggcgttgac gtgcaaggca cgtgcactgt ccgacgatca attgaccaa 840
292 ttacatgttg ccactgatgg taggtctagg ctttgccctc ctttgccacc aggttactta 900
294 ggaaatgttg tgttcacagg cacacctatg gcaaaaatcaa gtgaactttt acaagaacca 960
296 ttgacaaatt cagccaagag aattcatagt gcattatcaa aaatggatga caattaccta 1020
298 agatcagctc tgcattacct cgaattactg cccgatttat cggctttaat ccgtggaccg 1080
300 acgtactttg ctagccctaa tcttaatat aatagttgga ctagattgcc tgttcatgat 1140
302 tcagattttg gatggggaag gccaatcat atgggaccag cttgcatttt atatgaaggg 1200
304 acagtttata tattgccaag tccaaatagt aaagatagga acttgcgttt ggctgtttgt 1260
306 ttagatgctg atcacatgc acttttgag aaqtatttgt atgaattttg agaggttgaa 1320
308 aaaaaaatca agaattgtcc aacacttgag aattatctta ggtgtgggtg gttttggatt 1380
310 aaggcatttt gtaacttggt ttctattggt tttttggggg gtcagtttgt tttcaaaaaa 1440
312 aaaaaaaaaa aaaaaa 1456
315 <210> SEQ ID NO: 4
316 <211> LENGTH: 1293
317 <212> TYPE: DNA
318 <213> ORGANISM: Lycopersicon esculentum
320 <400> SEQUENCE: 4
321 atgggaagtg aaaaaatgat gaaaattaat atcaaagaat caacactagt gaaaccatca 60
323 aaaccaacac caacaaagag aatttggagt tctaatttgg atttaattgt tggagaatt 120
325 catcttttga ctgtttattt ttataaacca aatggatctt caaatttttt tgataataaa 180
327 gttattaaag aagcattaag taatgtttta gtttcatttt atccaatggc tggagatta 240
329 ggtagggatg aacaaggtag aattgaagtt aattgtaatg gtgaagggtg tttgtttggt 300
331 gaggtgaaa gtgattcatg tgttgatgat tttggtgatt ttacaccatc tttggaactt 360
333 agaaaaactca ttccaagtgt tgaaacctct ggagatatct caactttccc actagttata 420
335 tttcagatta ctcgtttcaa gtgtggcgga gtcgctcttg gtggtggagt attccacacg 480
337 ttatccgatg gtctctcatc catccacttc atcaacacgt ggtcggacat cgcccgtggc 540
339 ctctccgtcg cagtcgccgc gttcatcgat cggacgctcc tccgtgcaag ggaccaccg 600
341 acatattctt tgcagcacgt tgagtaccat cctccacctt cctaaaactc atcgaaaaat 660
343 cgcgagtcca gtaccacgac catgttgaaa ttctcgagtg aacaactcgg gcttcttaag 720
345 tccaagtcca aaaatgaggg tagcacctat gaaatcctcg cagcccatat ttggcgatgc 780
347 acgtgcaagg cacgtggatt gccagaggat caattgacca aattacacgt ggccaccgac 840
349 ggaaggtaa ggctttgccc tcccttgcca ccgggttacc taggaaacgt cgtgttcacg 900
351 gcaaccccaa tagctaaatc atgcgaactt caatcagagc cgttgacaaa ttccgtcaag 960
353 agaattcaca acgagttgat caaatggac gacaattacc taagatcagc actggattac 1020
355 ctcgatttac aacctgattt atcaacccta attcggggcc cggcttactt tgctagccct 1080
357 aacctcaata ttaatagttg gactaggttg cctgtccatg agtgtgattt tggatggggt 1140
359 aggccaaattc atatgggacc agcttgctatt ttatatgaag ggacaattta tattatacca 1200
361 agtccaaatt ctaaagatag gaacttgctt ttggctggtt gtctagatgc tggtcacatg 1260
363 tcactatttg aaaaaatatt atatgaatta tga 1293

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366 <210> SEQ ID NO: 5
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368 <212> TYPE: DNA
369 <213> ORGANISM: Artificial sequence
371 <220> FEATURE:
372 <223> OTHER INFORMATION: Oligonucleotide
374 <400> SEQUENCE: 5
375 gactcgagtc gacatcgatt tttttttttt ttttt 35
378 <210> SEQ ID NO: 6
379 <211> LENGTH: 35
380 <212> TYPE: DNA
381 <213> ORGANISM: Artificial sequence
383 <220> FEATURE:
384 <223> OTHER INFORMATION: Oligonucleotide
386 <400> SEQUENCE: 6
387 ccatgggaag tgaaaaaatg atgaaaatta atata 35
390 <210> SEQ ID NO: 7
391 <211> LENGTH: 35
392 <212> TYPE: DNA
393 <213> ORGANISM: Artificial sequence
395 <220> FEATURE:
396 <223> OTHER INFORMATION: Oligonucleotide
398 <400> SEQUENCE: 7
399 ggatcctcat aattcatata aatatttttc aaata 35
402 <210> SEQ ID NO: 8
403 <211> LENGTH: 29
404 <212> TYPE: DNA
405 <213> ORGANISM: Artificial sequence
407 <220> FEATURE:
408 <223> OTHER INFORMATION: Oligonucleotide
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414 <210> SEQ ID NO: 9
415 <211> LENGTH: 32
416 <212> TYPE: DNA
417 <213> ORGANISM: Artificial sequence
419 <220> FEATURE:
420 <223> OTHER INFORMATION: Oligonucleotide
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427 <211> LENGTH: 17
428 <212> TYPE: DNA
429 <213> ORGANISM: Artificial sequence
431 <220> FEATURE:
432 <223> OTHER INFORMATION: Oligonucleotide
434 <400> SEQUENCE: 10
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438 <210> SEQ ID NO: 11

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VERIFICATION SUMMARY

DATE: 03/03/2006

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